

### LISTING OF THE CLAIMS

The following listing of the claims replaces all prior versions and listings of claims for this application. Within the following listing of the claims, claims 1-16 are canceled and claims 17-92 are new.

1-16. **(Canceled)**

17. **(New)** A method of calculating a patient's relative risk (RR) for adverse drug reactions (ADRs) from statin therapy by genotyping a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for three possible genotypes of each SNP, the relative risk associate with each genotype is calculated as follows:

$$RR\ 1 = \frac{N\ 11}{N\ 21} \bigg/ \frac{N\ 12 + N\ 13}{N\ 22 + N\ 23}$$

$$RR\ 2 = \frac{N\ 12}{N\ 22} \bigg/ \frac{N\ 11 + N\ 13}{N\ 21 + N\ 23}$$

$$RR\ 3 = \frac{N\ 13}{N\ 23} \bigg/ \frac{N\ 11 + N\ 12}{N\ 21 + N\ 22}$$

wherein:

RR1 represents the relative risk for genotype 1;

RR2 represents the relative risk for genotype 2;

RR3 represents the relative risk for genotype 3;

N11 represents genotype 1, N12 represents genotype 2, and N13 represents genotype 3 for a population of patients that are being tested for ADRs from statin therapy;

N21 represents genotype 1, N22 represents genotype 2, and N23 represents genotype 3 for a population of patients that are known not to be at risk for ADRs from statin therapy;

a value of  $RR1 > 1$  indicates an increased risk for ADRs from statin therapy for individuals carrying genotype 1;

a value of  $RR2 > 1$  indicates an increased risk for ADRs from statin therapy for individuals carrying genotype 2; and

a value of  $RR3 > 1$  indicates an increased risk for ADRs from statin therapy for individuals carrying genotype 3.

18. **(New)** The method of claim 17, wherein genotype 1, genotype 2, and genotype 3 represent a single nucleotide polymorphism (SNP).

19. **(New)** The method of claim 18, wherein the SNP is a C to T SNP.

20. **(New)** The method of claim 19, wherein genotype 1, genotype 2, and genotype 3 are CC, TT, and CT.

21. **(New)** The method of claim 18, wherein the SNP is an A to G SNP.

22. **(New)** The method of claim 21, wherein genotype 1, genotype 2, and genotype 3 are AA, AG, and GG.

23. **(New)** The method of claim 18, wherein the SNP is a C to G SNP.

24. **(New)** The method of claim 23, wherein genotype 1, genotype 2, and genotype 3 are CC, CG, and GG.

25. **(New)** The method of claim 18, wherein the SNP is an A to T SNP.

26. **(New)** The method of claim 25, wherein genotype 1, genotype 2, and genotype 3 are AA, AT, and TT.

27. **(New)** The method of claim 18, wherein the SNP is a G to T SNP.

28. **(New)** The method of claim 27, wherein genotype 1, genotype 2, and genotype 3 are GG, GT, and TT.

29. **(New)** The method of claim 18, wherein the SNP is an A to C SNP.

30. **(New)** The method of claim 29, wherein genotype 1, genotype 2, and genotype 3 are AA, AC, and CC.

31. **(New)** A method of calculating a patient's relative risk (RR) for adverse drug reactions (ADRs) from statin therapy by determining allele frequency in a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for two possible alleles of each SNP, the relative risk associate with each allele is calculated as follows:

$$RR_1 = \frac{N_{11}}{N_{21}} \bigg/ \frac{N_{12}}{N_{22}}$$

$$RR_2 = \frac{N_{12}}{N_{22}} \bigg/ \frac{N_{11}}{N_{21}}$$

wherein:

RR1 represents the relative risk for allele 1;

RR2 represents the relative risk for allele 2;

N11 represents allele 1 and N12 represents allele 2 for a population of patients that are being tested for ADRs from statin therapy;

N21 represents allele 1 and N22 represents allele 2 for a population of patients that are known not to be at risk for ADRs from statin therapy;

a value of  $RR_1 > 1$  indicates an increased risk for ADRs from statin therapy for individuals carrying allele 1; and

a value of  $RR_2 > 1$  indicates an increased risk for ADRs from statin therapy for individuals carrying allele 2.

32. **(New)** The method of claim 31, wherein allele 1 and allele 2 are independently selected from A, C, T, and G.

33. **(New)** The method of claim 32, wherein allele 1 and allele 2 are C and T, respectively.

34. **(New)** The method of claim 32, wherein allele 1 and allele 2 are A and G, respectively.

35. **(New)** The method of claim 32, wherein allele 1 and allele 2 are A and T, respectively.

36. **(New)** The method of claim 32, wherein allele 1 and allele 2 are C and G, respectively.

37. **(New)** The method of claim 32, wherein allele 1 and allele 2 are A and C, respectively.

38. **(New)** The method of claim 32, wherein allele 1 and allele 2 are G and T, respectively.

39. **(New)** The method of claims 17 and 31, wherein patients with  $RR1 < 1$ ,  $RR2 < 1$ , or  $RR3 < 1$  should receive low doses of statins or switch to alternative therapies to avoid ADRs.

40. **(New)** A method of calculating a patient's relative risk (RR) for being a high responder to statin therapy by genotyping a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for three possible genotypes of each SNP, the relative risk associate with each genotype is calculated as follows:

$$RR\ 1 = \frac{N\ 11}{N\ 21} \bigg/ \frac{N\ 12 + N\ 13}{N\ 22 + N\ 23}$$

$$RR\ 2 = \frac{N\ 12}{N\ 22} \bigg/ \frac{N\ 11 + N\ 13}{N\ 21 + N\ 23}$$

$$RR\ 3 = \frac{N\ 13}{N\ 23} \bigg/ \frac{N\ 11 + N\ 12}{N\ 21 + N\ 22}$$

wherein:

RR1 represents the relative risk for genotype 1;

RR2 represents the relative risk for genotype 2;

RR3 represents the relative risk for genotype 3;

N11 represents genotype 1, N12 represents genotype 2, and N13 represents genotype 3 for a population of patients that are being tested for high response to statin therapy;

N21 represents genotype 1, N22 represents genotype 2, and N23 represents genotype 3 for a population of patients that are low responders statin therapy;

a value of  $RR1 > 1$  indicates an increased risk for being a high responder to statin therapy for individuals carrying genotype 1;

a value of  $RR2 > 1$  indicates an increased risk for being a high responder to statin therapy for individuals carrying genotype 2; and

a value of  $RR > 1$  indicates an increased risk for being a high responder to statin therapy individuals carrying genotype 3.

41. **(New)** The method of claim 40, wherein genotype 1, genotype 2, and genotype 3 represent a single nucleotide polymorphism (SNP).

42. **(New)** The method of claim 41, wherein the SNP is a C to T SNP.

43. **(New)** The method of claim 42, wherein genotype 1, genotype 2, and genotype 3 are CC, TT, and CT.

44. **(New)** The method of claim 41, wherein the SNP is an A to G SNP.

45. **(New)** The method of claim 44, wherein genotype 1, genotype 2, and genotype 3 are AA, AG, and GG.

46. **(New)** The method of claim 41, wherein the SNP is a C to G SNP.

47. **(New)** The method of claim 46, wherein genotype 1, genotype 2, and genotype 3 are CC, CG, and GG.

48. **(New)** The method of claim 41, wherein the SNP is an A to T SNP.

49. **(New)** The method of claim 48, wherein genotype 1, genotype 2, and genotype 3 are AA, AT, and TT.

50. **(New)** The method of claim 41, wherein the SNP is a G to T SNP.

51. **(New)** The method of claim 50, wherein genotype 1, genotype 2, and genotype 3 are GG, GT, and TT.

52. **(New)** The method of claim 41, wherein the SNP is an A to C SNP.

53. **(New)** The method of claim 52, wherein genotype 1, genotype 2, and genotype 3 are AA, AC, and CC.

54. **(New)** A method of calculating a patient's relative risk (RR) for being a high responder to statin therapy by determining allele frequency in a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for two possible alleles of each SNP, the relative risk associate with each allele is calculated as follows:

$$RR_1 = \frac{N_{11}}{N_{21}} \bigg/ \frac{N_{12}}{N_{22}}$$

$$RR_2 = \frac{N_{12}}{N_{22}} \bigg/ \frac{N_{11}}{N_{21}}$$

wherein:

RR1 represents the relative risk for allele 1;

RR2 represents the relative risk for allele 2;

N11 represents allele 1 and N12 represents allele 2 for a population of patients that are being tested for high response to statin therapy;

N21 represents allele 1 and N22 represents allele 2 for a population of patients that are known to be low responders to statin therapy;

a value of  $RR_1 > 1$  indicates an increased risk for being a high responder to statin therapy for individuals carrying allele 1; and

a value of  $RR_2 > 1$  indicates an increased risk for being a high responder to statin therapy for individuals carrying allele 2.

55. **(New)** The method of claim 54, wherein allele 1 and allele 2 are independently selected from A, C, T, and G.

56. **(New)** The method of claim 55, wherein allele 1 and allele 2 are C and T, respectively.

57. **(New)** The method of claim 55, wherein allele 1 and allele 2 are A and G, respectively.

58. **(New)** The method of claim 55, wherein allele 1 and allele 2 are A and T, respectively.

59. **(New)** The method of claim 55, wherein allele 1 and allele 2 are C and G, respectively.

60. **(New)** The method of claim 55, wherein allele 1 and allele 2 are A and C, respectively.

61. **(New)** The method of claim 55, wherein allele 1 and allele 2 are G and T, respectively.

62. **(New)** The method of claims 31 and 54, wherein patients with  $RR1 < 1$ ,  $RR2 < 1$ , or  $RR3 < 1$  should receive low doses of statins in order to avoid adverse drug reactions.

63. **(New)** A method of calculating a patient's relative risk (RR) for cardiovascular disease (CVD) by genotyping a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for three possible genotypes of each SNP, the relative risk associate with each genotype is calculated as follows:

$$RR\ 1 = \frac{N\ 11}{N\ 21} \bigg/ \frac{N\ 12 + N\ 13}{N\ 22 + N\ 23}$$

$$RR\ 2 = \frac{N\ 12}{N\ 22} \bigg/ \frac{N\ 11 + N\ 13}{N\ 21 + N\ 23}$$

$$RR\ 3 = \frac{N\ 13}{N\ 23} \bigg/ \frac{N\ 11 + N\ 12}{N\ 21 + N\ 22}$$

wherein:

RR1 represents the relative risk for genotype 1;

RR2 represents the relative risk for genotype 2;

RR3 represents the relative risk for genotype 3;

N11 represents genotype 1, N12 represents genotype 2, and N13 represents genotype 3 for a population of patients that are being tested for CVD;

N21 represents genotype 1, N22 represents genotype 2, and N23 represents genotype 3 for a population of patients that are known not to be at risk for CVD;

a value of  $RR1 > 1$  indicates an increased risk for CVD for individuals carrying genotype 1;

a value of  $RR2 > 1$  indicates an increased risk for CVD for individuals carrying genotype 2; and

a value of  $RR3 > 1$  indicates an increased risk for CVD for individuals carrying genotype 3.

64. **(New)** The method of claim 62, wherein genotype 1, genotype 2, and genotype 3 represent a single nucleotide polymorphism (SNP).

65. **(New)** The method of claim 64, wherein the SNP is a C to T SNP.

66. **(New)** The method of claim 65, wherein genotype 1, genotype 2, and genotype 3 are CC, TT, and CT.

67. **(New)** The method of claim 64, wherein the SNP is an A to G SNP.

68. **(New)** The method of claim 67, wherein genotype 1, genotype 2, and genotype 3 are AA, AG, and GG.

69. **(New)** The method of claim 64, wherein the SNP is a C to G SNP.

70. **(New)** The method of claim 69, wherein genotype 1, genotype 2, and genotype 3 are CC, CG, and GG.

71. **(New)** The method of claim 64, wherein the SNP is an A to T SNP.

72. **(New)** The method of claim 71, wherein genotype 1, genotype 2, and genotype 3 are AA, AT, and TT.

73. **(New)** The method of claim 64, wherein the SNP is a G to T SNP.

74. **(New)** The method of claim 73, wherein genotype 1, genotype 2, and genotype 3 are GG, GT, and TT.

75. **(New)** The method of claim 64, wherein the SNP is an A to C SNP.

76. **(New)** The method of claim 75, wherein genotype 1, genotype 2, and genotype 3 are AA, AC, and CC.



77. **(New)** A method of calculating a patient's relative risk (RR) for cardiovascular disease (CVD) by determining allele frequency in a single nucleotide polymorphism (SNP) in DNA of the patient, wherein for two possible alleles of each SNP, the relative risk associate with each allele is calculated as follows:

$$RR_1 = \frac{N_{11}}{N_{21}} \bigg/ \frac{N_{12}}{N_{22}}$$

$$RR_2 = \frac{N_{12}}{N_{22}} \bigg/ \frac{N_{11}}{N_{21}}$$

wherein:

RR1 represents the relative risk for allele 1;

RR2 represents the relative risk for allele 2;

N11 represents allele 1 and N12 represents allele 2 for a population of patients that are being tested for CVD;

N21 represents allele 1 and N22 represents allele 2 for a population of patients that are known not to be at risk for CVD;

a value of  $RR_1 > 1$  indicates an increased risk for CVD for individuals carrying allele 1; and

a value of  $RR_2 > 1$  indicates an increased risk for CVD for individuals carrying allele 2.

78. **(New)** The method of claim 77, wherein allele 1 and allele 2 are independently selected from A, C, T, and G.

79. **(New)** The method of claim 78, wherein allele 1 and allele 2 are C and T, respectively.

80. **(New)** The method of claim 78, wherein allele 1 and allele 2 are A and G, respectively.

81. **(New)** The method of claim 78, wherein allele 1 and allele 2 are A and T, respectively.

82. **(New)** The method of claim 78, wherein allele 1 and allele 2 are C and G, respectively.

83. **(New)** The method of claim 78, wherein allele 1 and allele 2 are A and C, respectively.

84. **(New)** The method of claim 78, wherein allele 1 and allele 2 are G and T, respectively.

85. **(New)** The method of claim 19, wherein the C to T SNP is genotyped using oligonucleotide primers of SEQ ID NOs: 1-4 (baySNP 160).

86. **(New)** The method of claim 21, wherein the A to G SNP is genotyped with oligonucleotide primers selected from the group consisting of SEQ ID NOs: 37-40 (baySNP 4564); SEQ ID NOs: 41-44 (baySNP 5569); and SEQ ID NOs: 65-68 (baySNP 12399).

87. **(New)** The method of claim 29, wherein the A to C SNP is genotyped using oligonucleotide primers of SEQ ID NOs: 33 to 36 (baySNP 3907).

88. **(New)** The method of claim 42, wherein the C to T SNP is genotyped using oligonucleotide primers of SEQ ID NOs: 57-60 (baySNP 8589).

89. **(New)** The method of claim 65, wherein the C to T SNP is genotyped with oligonucleotide primers selected from the group consisting of SEQ ID NOs: 9-12 (baySNP 1371); SEQ ID NOs: 17-20 (baySNP 2178); SEQ ID NOs: 21-24 (baySNP 2198); and SEQ ID NOs: 29-32 (baySNP 2267).

90. **(New)** The method of claim 67, wherein the A to G SNP is genotyped with oligonucleotide primers selected from the group consisting of SEQ ID NOs: 5-8 (baySNP 1278); SEQ ID NOs: 13-16 (baySNP 1806); SEQ ID NOs: 45-48 (baySNP 6872); and SEQ ID NOs: 53-56 (baySNP 8242).

91. **(New)** The method of claim 69, wherein the C to G SNP is genotyped using oligonucleotide primers of SEQ ID NOs: 61-64 (baySNP 10771).

92. **(New)** The method of claim 71, wherein the A to T SNP is genotyped with oligonucleotide primers selected from SEQ ID NOs: 25-28 (baySNP 2214) and SEQ ID NOs: 49-52 (baySNP 8164).